

REMARKS

Claims 15 through 25 have been canceled by amendment herein, without prejudice or disclaimer to their reintroduction in subsequent applications. Accordingly, claims 1-14 and 26-30 are pending.

Applicants expressly reserve their right under 35 USC §121 to file one or more continuation of divisional applications directed to the subject matter of any canceled claims during the pendency of this application.

Respectfully submitted,

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Currently Pending Claims

1. A method for identifying a gene; wherein the method comprises:
 - (a) obtaining a putative gene sequence (PGS);
 - (b) contacting a cell with a zinc finger protein, wherein the cell comprises the putative gene sequence, and wherein the zinc finger protein binds to and modulates expression of the putative gene sequence; and
 - (c) assaying the cell for at least one selected phenotype;wherein, if one or more of the selected phenotypes are observed, the putative gene sequence is identified as a gene.
2. The method of claim 1, wherein the gene encodes a protein.
3. The method of claim 1, wherein the gene encodes a RNA selected from the group consisting of structural RNA, regulatory RNA, enzymatic RNA, antisense RNA, ribozyme, ribosomal RNA and transfer RNA.
4. The method of claim 1, wherein the zinc finger protein comprises three or more zinc finger binding domains.
5. The method of claim 1, wherein the zinc finger protein binds near the putative transcription startsite of the PGS.
6. The method of claim 1, wherein the zinc finger protein binds in the putative transcribed region of the PGS.
7. The method of claim 6, wherein the zinc finger protein binds in the putative coding region of the PGS.
8. The method of claim 1, wherein the zinc finger protein binds in a putative nontranscribed regulatory region of the PGS.
9. The method of claim 1, wherein the zinc finger protein comprises an activation domain.
10. The method of claim 9, wherein the activation domain is selected from the group consisting of VP16, p65 and functional fragments thereof.
11. The method of claim 1, wherein the zinc finger protein comprises a repression domain.
12. The method of claim 11, wherein the repression domain is selected from the group consisting of KRAB, v-erbA and functional fragments thereof.

13. The method of claim 1, wherein the zinc finger protein comprises a bifunctional domain (BFD), wherein the activity of the bifunctional domain is dependent upon interaction of the BFD with a second molecule.

14. The method of claim 13, wherein the BFD is selected from the group consisting of thyroid hormone receptor, retinoic acid receptor, estrogen receptor and glucocorticoid receptor.

15 to 25. *Canceled.*

26. The method of claim 1, wherein the cell is infected with a virus.

27. The method of claim 26, wherein the gene is a viral gene.

28. The method of claim 1, wherein the putative gene sequence is obtained from a gene prediction algorithm.

29. The method of claim 1, wherein the putative gene sequence is obtained by analysis of expressed sequence tags.

30. The method of claim 1, wherein the putative gene sequence is obtained by homology.